

10/581551

JAP20 Rec'd PCT/PTO 02 JUN 2006

SEQUENCE LISTING

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<120> Fluorescent protein

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
Lys Thr Thr Tyr Lys Ala Ala Lys Ile Leu Lys Met Pro Gly Ser
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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35 40 45

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Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
180 185 190
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

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Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp

145 150 155 160

Thr Leu Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met

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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser

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35 40 45

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Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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Glu Phe Glu Asp Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
145 150 155 160
acg ttg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa atg 528
Thr Leu Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met
165 170 175
aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
180 185 190
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
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Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp

145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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35 40 45
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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
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 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
 145 150 155 160
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa atg 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met
 165 170 175
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
 180 185 190
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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20 25 30

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

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85	90	95	
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
180	185	190	
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
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Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

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Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

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95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe

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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		
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Arg Pro Tyr Glu Gly His Gln Glu Leu Thr Leu Arg Val Thr Met Ala		
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Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe		
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Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp		
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
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Trp Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

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60

Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

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75

80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

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90

95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe

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Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
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 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
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 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
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 Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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 Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
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 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
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Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
Cys Tyr Gly His Arg Ala Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
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Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

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Glu Leu Val Glu Asp Ala Val Ala His Ser

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

tgt tac ggc cac aga gct ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Ala Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85	90	95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336		
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu		
100	105	110.
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384		
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe		
115	120	125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro		
130	135	140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val		
145	150	155
160		
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe		
165	170	175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576		
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp		
180	185	190
cat tac atc ggg cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624		
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		
195	200	205
gag ctg gta gaa gat gca gta gct cat tcc taa 657		
Glu Leu Val Glu Asp Ala Val Ala His Ser		
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<212> PRT

<213> Fungia sp.

<400> 15

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
Cys Tyr Gly His Arg Ser Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215
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 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 tgt tac ggc cac aga tct ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Ser Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215
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<211> 218
<212> PRT

<213> Fungia sp.

<400> 17

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195	200	205
Glu Leu Val Glu Asp Ala Val Ala His Ser		
210	215	
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1	5	10
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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96		
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly		
20	25	30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144		
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala		
35	40	45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192		
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe		
50	55	60
tgt tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240		
Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp		
65	70	75
80		
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288		
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu		
85	90	95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336		

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215
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<213> Fungia sp.

<400> 19

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Thr Gly
20 25 30
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210 215

<210> 20

<211> 657

<212> DNA

<213> Fungia sp.

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

tgt tac ggc cac aga act ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215
<210> 21
<211> 218
<212> PRT
<213> Fungia sp.
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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Glu Leu Val Glu Asp Ala Val Ala His Ser

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<211> 657

<212> DNA

<213> Fungia sp.

<400> 22

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

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<212> DNA

<213> Fungia sp.

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga ctt ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
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20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

<210> 26

<211> 657

<212> DNA

<213> Fungia sp.

<400> 26

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga tac ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa			657
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
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<213> Fungia sp.			
<400> 27			
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp			
1	5	10	15
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			

20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

<210> 28

<211> 657

<212> DNA

<213> Fungia sp.

<400> 28

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga cag ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115

120

125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205
gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
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<223> unknown amiono acid
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp
180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser

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215

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<211> 657

<212> DNA

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<220>

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<222> (556)

<223> unknown nucleotide

<400> 30

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga aat ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85	90	95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336		
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu		
100	105	110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384		
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe		
115	120	125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro		
130	135	140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val		
145	150	155
160		
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe		
165	170	175
aag act act tac aag gcg gca aaa gag ntt ctt gaa atg cca gga gac 576		
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp		
180	185	190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624		
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		
195	200	205
gag ctg gta gaa gat gca gta gct cat tcc taa 657		
Glu Leu Val Glu Asp Ala Val Ala His Ser		
210	215	
<210> 31		
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<212> PRT

<213> Fungia sp.

<400> 31

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
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Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
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Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
35 40 45
Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
50 55 60
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65 70 75 80
Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
85 90 95
Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
100 105 110
Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
115 120 125
Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
130 135 140
Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145 150 155 160
Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
165 170 175
Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
180 185 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
195 200 205
Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
210 215 220
Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225 230 235 240
Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
245 250 255
Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
260 265 270
Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
275 280 285
Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
290 295 300
Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305 310 315 320
Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gln
325 330 335
Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
340 345 350
Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Asn
355 360 365
Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
370 375 380
Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385 390 395 400
Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser

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405	410	415
Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val		
420	425	430
Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met		
435	440	445
Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly		
450	455	460
Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg		
465	470	475
Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu		
485	490	495
Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys		
500	505	510
Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr		
515	520	525
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu		
530	535	540
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg		
545	550	555
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro		
565	570	575
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser		
580	585	590
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr		
595	600	605
Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe Lys		
610	615	620

Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His
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 Leu Val Glu Asp Ala Val Ala His Ser
 660 665
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 <212> DNA
 <213> Fungia sp.
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 Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
 1 5 10 15
 acg tac ggg ttg ggg gac agg aaa gat cag ggg ggc tac acc atg cac 96
 Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
 20 25 30
 caa gac caa gag ggt gac acg gac gct ggc ctg aaa gaa tct ccc ctg 144
 Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
 35 40 45
 cag acc ccc act gag gac gga tct gag gaa ccg ggc tct gaa acc tct 192
 Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
 50 55 60
 gat gct aag agc act cca aca gcg gaa gat gtg aca gca ccc tta gtg 240
 Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
 65 70 75 80
 gat gag gga gct ccc ggc aag cag gct gcc gcg cag ccc cac acg gag 288

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
85 90 95
atc cca gaa gga acc aca gct gaa gaa gca ggc att gga gac acc ccc 336
Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
100 105 110
agc ctg gaa gac gaa gct gct ggt cac gtg acc caa gct cgc atg gtc 384
Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
115 120 125
agt aaa agc aaa gac ggg act gga agc gat gac aaa aaa gcc aag ggg 432
Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
130 135 140
gct gat ggt aaa acg aag atc gcc aca ccg cggt gga gca gcc cct cca 480
Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145 150 155 160
ggc cag aag ggc cag gcc aac gcc acc agg att cca gca aaa acc ccg 528
Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
165 170 175
ccc gct cca aag aca cca ccc agc tct ggt gaa cct cca aaa tca ggg 576
Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
180 185 190
gat cgc agc ggc tac agc agc ccc ggc tcc cca ggc act ccc ggc agc 624
Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
195 200 205
cgc tcc cgc acc ccg tcc ctt cca acc cca ccc acc cgg gag ccc aag 672
Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
210 215 220
aag gtg gca gtg gtc cgt act cca ccc aag tcg ccg tct tcc gcc aag 720

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225 230 235 240
agc cgc ctg cag aca gcc ccc gtg ccc atg cca gac ctg aag aat gtc 768
Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
245 250 255
aag tcc aag atc ggc tcc act gag aac ctg aag cac cag ccg gga ggc 816
Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
260 265 270
ggg aag gtg cag ata att aat aag aag ctg gat ctt agc aac gtc cag 864
Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
275 280 285
tcc aag tgt ggc tca aag gat aat atc aaa cac gtc ccg gga ggc ggc 912
Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
290 295 300
agt gtg caa ata gtc tac aaa cca gtt gac ctg agc aag gtg acc tcc 960
Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305 310 315 320
aag tgt ggc tca tta ggc aac atc cat cat aaa cca gga ggt ggc cag 1008
Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gln
325 330 335
gtg gaa gta aaa tct gag aag ctt gac ttc aag gac aga gtc cag tcg 1056
Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
340 345 350
aag att ggg tcc ctg gac aat atc acc cac gtc cct ggc gga gga aat 1104
Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Asn
355 360 365
aaa aag att gaa acc cac aag ctg acc ttc cgc gag aac gcc aaa gcc 1152

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
370 375 380
aag aca gac cac ggg gcg gag atc gtg tac aag tcg cca gtg gtg tct 1200
Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385 390 395 400
ggg gac acg tct cca cgg cat ctc agc aat gtc tcc tcc acc ggc agc 1248
Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
405 410 415
atc gac atg gta gac tcg ccc cag ctc gcc acg cta gct gac gag gtg 1296
Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
420 425 430
tct gcc tcc ctg gcc aag cag ggt ttg gga tcc gga ggt gaa ttc atg 1344
Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met
435 440 445
gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac ggc 1392
Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly
450 455 460
tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc aga 1440
Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg
465 470 475 480
cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc gag 1488
Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu
485 490 495
ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc tgt 1536
Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys
500 505 510
tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac tat 1584

Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr
 515 520 525
 ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg gag 1632
 Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu
 530 535 540
 ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt aga 1680
 Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg
 545 550 555 560
 gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt cct 1728
 Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro
 565 570 575
 gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca tca 1776
 Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser
 580 585 590
 acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt acg 1824
 Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr
 595 600 605
 atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc aag 1872
 Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe Lys
 610 615 620
 act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac cat 1920
 Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His
 625 630 635 640
 tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act gag 1968
 Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu
 645 650 655
 ctg gta gaa gat gca gta gct cat tcc taa 1998

Leu Val Glu Asp Ala Val Ala His Ser

660 665

<210> 33

<211> 480

<212> PRT

<213> Fungia sp.

<400> 33

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20 25 30

Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn

35 40 45

Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp

50 55 60

Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val

65 70 75 80

Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg

85 90 95

Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu

100 105 110

Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg

115 120 125

Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys

130 135 140

Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val

145 150 155 160

Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser
165 170 175
Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met
180 185 190
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn
195 200 205
Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp
210 215 220
Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys
225 230 235 240
Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg
245 250 255
Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys
260 265 270
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
275 280 285
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
290 295 300
Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp
305 310 315 320
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr
325 330 335
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
340 345 350
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
355 360 365
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys

370	375	380	
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
385	390	395	400
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly			
405	410	415	
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly			
420	425	430	
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile			
435	440	445	
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys			
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Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser			
465	470	475	480
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atg aag gct gcg ccc atg aaa gaa gca aac gtc cac gga caa ggc aac 96			
Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn			
20	25	30	
ttg gcc tac cca gct gtg cggtt acc cat ggg act ctg gag agc gtg aat 144			
Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn			
35	40	45	

ggg ccc agg gca ggt tcg aga ggt ctg acg acg tcc ctg gct gac 192
 Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Ser Leu Ala Asp
 50 55 60
 act ttt gag cac gtg atc gaa gag ctg ctg gat gag gac cag aag gtt 240
 Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val
 65 70 75 80
 cg^g ccc aac gaa gaa aac cat aag gac gc^g gac ttg tac act tcc cg^g 288
 Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg
 85 90 95
 gtg atg ctc agc agt caa gtg cct ttg gag cct cct ctg ctc ttt ctg 336
 Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu
 100 105 110
 ctg gag gaa tac aaa aat tac ctg gat gcc gca aac atg tct atg agg 384
 Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg
 115 120 125
 gtt cg^g cg^c cac tcc gac ccc gcc cg^c cgt gg^g gag ctg agc gtg tgt 432
 Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys
 130 135 140
 gac agt att agc gag tgg gtc aca gc^g gca gat aaa aag act gca gtg 480
 Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val
 145 150 155 160
 gac atg tcc ggt gg^g acg gtc aca gtc ctg gag aaa gtc ccg gta tca 528
 Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser
 165 170 175
 aaa ggc caa ctg aag caa tat ttc tac gag acc aag tgt aat ccc atg 576
 Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met
 180 185 190

ggt tac acg aag gaa ggc tgc agg ggc ata gac aaa agg cac tgg aac 624
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn
195 200 205
tcg caa tgc cga act acc caa tcg tat gtt cggtt gcc ctt act atg gat 672
Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp
210 215 220
agc aaa aag aga att ggc tgg cggtt ttc ata agg ata gac act tcc tgt 720
Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys
225 230 235 240
gta tgt aca ctg acc att aaa agg gga aga ggg gta ccg cggtt gcc cggtt 768
Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg
245 250 255
gac cca ccg gtc gcc acc atg gtg agt gtg att aaa cca gag atg aag 816
Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys
260 265 270
atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 864
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
275 280 285
gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 912
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
290 295 300
cta cgc gtc aca atg gcc gag ggc ggg cca atg cct ttc gcg ttt gac 960
Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp
305 310 315 320
tta gtg tca cac gtg ttc tgt tac ggc cac aga gta ttt act aaa tat 1008
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr
325 330 335

cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1056
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
340 345 350
tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1104
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
355 360 365
agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1152
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
370 375 380
ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1200
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
385 390 395 400
agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1248
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
405 410 415
gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1296
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly
420 425 430
aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa gag att 1344
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile
435 440 445
ctt gaa atg cca gga gac cat tac atc ggc cat cgc ctc gtc agg aaa 1392
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys
450 455 460
acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1440
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
465 470 475 480

taa 1443
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 <211> 464
 <212> PRT
 <213> Fungia sp.
 <400> 35

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 20 25 30
 Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
 35 40 45
 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
 Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110
 Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160
 Arg Gly Asp Val Thr Gln Phe Leu Leu Glu Gly Gly Tyr Gln

	165	170	175
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met			
	180	185	190
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly			
	195	200	205
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu His Ala Glu Ala			
	210	215	220
His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val			
	225	230	240
Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys			
	245	250	255
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile			
	260	265	270
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr			
	275	280	285
Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp			
	290	295	300
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr			
	305	310	320
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu			
	325	330	335
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val			
	340	345	350
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys			
	355	360	365
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
	370	375	380

Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
 450 455 460
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 tac cgt atg gaa ggc agt gtc aat ggc cat gaa ttc acg atc gaa ggt 96
 Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
 20 25 30
 gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144
 Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
 35 40 45
 atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192
 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60

tca aca gcc ttt caa tat gga aac aga tgc ttc aca aag tac cct gca 240
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
65 70 75 80
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat 288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
85 90 95
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg 336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
100 105 110
agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat 384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
115 120 125
ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att 432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
130 135 140
ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
145 150 155 160
aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac cag 528
Arg Gly Asp Val Thr Gln Phe Leu Leu Glu Gly Gly Tyr Gln
165 170 175
aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg 576
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
180 185 190
ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
195 200 205

caa act gca aaa ggc ttc aag gtc aag ctg gaa cat gct gag gct 672
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
210 215 220
cat gtt aac cct ttg aag gtt aaa ggt ggc agc ggt ggc gac gag gtg 720
His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val
225 230 235 240
gac ggt acc ggt ggc agc atg gtg agt gtg att aaa cca gag atg aag 768
Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys
245 250 255
atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 816
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
260 265 270
gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 864
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
275 280 285
cta cgc gtc aca atg gcc aag ggc ggg cca atg cct ttc gcg ttt gac 912
Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp
290 295 300
tta gtg tca cac gtg ttc tgt tac ggc cac aga cct ttt act aaa tat 960
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr
305 310 315 320
cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1008
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
325 330 335
tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1056
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Ser Ala Ser Val
340 345 350

agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1104
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 355 360 365
 ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1152
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 370 375 380
 agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1200
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400
 gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1248
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415
 aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa aag att 1296
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430
 ctt aaa atg cca gga agc cat tac atc agc cat cgc ctc gtc agg aaa 1344
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445
 acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1392
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
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 <213> Montipora. sp
 <400> 37

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Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly

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acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96		
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys		
20	25	30
cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggt gga 144		
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly		
35	40	45
cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac gga 192		
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly		
50	55	60
agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag 240		
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys		
65	70	75
cag tca ttc cct gag gga tat aca tgg gag agg atc atg cac ttt gaa 288		
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu		
85	90	95
gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336		
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn		
100	105	110

tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc aat 384
Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn
115 120 125
gga cct gtt atg cag aag aca cag ggc tgg gaa ccc aac act gag 432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
130 135 140
cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct 480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160
ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act 528
Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175
tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac 576
Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
180 185 190
cgc aaa ctg gat gta acc agt cac aac aag gat tac aca ttt gtt gag 624
Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
195 200 205
cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 666
Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
210 215 220
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<211> 222
<212> PRT
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Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

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Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly			
35	40	45	
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr			
50	55	60	
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val			
65	70	75	80
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe			
85	90	95	
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly			
100	105	110	
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro			
115	120	125	
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met			
145	150	155	160
Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
165	170	175	
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val			
180	185	190	
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly			
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<212> DNA

<213> *Montipora. sp*

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1

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15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

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25

30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

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40

45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr

50

55

60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65

70

75

80

aag cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe

85

90

95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100

105

110

aac tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125
 aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat ttt atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt 576
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
 180 185 190
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 gag cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220
 <210> 41
 <211> 222
 <212> PRT
 <213> *Montipora. sp*
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 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
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Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
35 40 45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr
50 55 60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
85 90 95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
100 105 110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
115 120 125

Asn Gly Pro Val Met Gln Lys Thr Gln Gly Trp Glu Pro Ser Thr
130 135 140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
145 150 155 160

Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
165 170 175

Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
180 185 190

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
195 200 205

Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
210 215 220

<210> 42

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 42

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1

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15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

20

25

30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

35

40

45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr

50

55

60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65

70

75

80

aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe

85

90

95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100

105

110

aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro

115 120 125

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr

130 135 140

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met

145 150 155 160

gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528
Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser

165 170 175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile

180 185 190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val

195 200 205

gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

210 215 220

<210> 43

<211> 222

<212> PRT

<213> *Montipora. sp*

<400> 43

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

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Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr		
50	55	60
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val		
65	70	75
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe		
85	90	95
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly		
100	105	110
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro		
115	120	125
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr		
130	135	140
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met		
145	150	155
Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser		
165	170	175
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile		
180	185	190
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val		
195	200	205
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly		
210	215	220
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<212> DNA

<213> *Montipora. sp*

<400> 44

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Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

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15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

20

25

30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

35

40

45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg atg tgt tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr

50

55

60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65

70

75

80

aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe

85

90

95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100

105

110

aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro

115

120

125

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576
 Thr Tyr Lys Ala Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220
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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
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Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
35 40 45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
50 55 60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
65 70 75 80

Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln
85 90 95

Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
100 105 110

Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
115 120 125

Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
130 135 140

Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
145 150 155 160

Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
165 170 175

Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
180 185 190

Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
195 200 205

Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
210 215 220

Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
225 230 235 240

Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

245	250	255
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp		
20	25	30
ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144		
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met		
35	40	45
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192		
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys		
50	55	60
gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240		
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys		
65	70	75
ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ttc cag 288		
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln		
85	90	95
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336		
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr		
100	105	110

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Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn

115 120 125

ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln

130 135 140

ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro

145 150 155 160

ccc aat gga cct gtt atg cag aag aca cag ggc tgg gaa ccc agc 528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser

165 170 175

act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr

180 185 190

atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys

195 200 205

tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu

210 215 220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser

225 230 235 240

gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

245 250 255

<210> 47

<211> 255

<212> PRT

<213> *Montipora. sp*

<400> 47

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20

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30

Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met

35

40

45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys

50

55

60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys

65

70

75

80

Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln

85

90

95

Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr

100

105

110

Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn

115

120

125

Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln

130

135

140

Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro

145

150

155

160

Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser

165

170

175

Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
180 185 190

Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
195 200 205

Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
210 215 220

Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
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<210> 48

<211> 765

<212> DNA

<213> *Montipora. sp*

<400> 48

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ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp

20 25 30

ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144

Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met

35 40 45

tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys

50 55 60

gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
65 70 75 80
ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ctt cag 288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln
85 90 95
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
100 105 110
ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
115 120 125
ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
130 135 140
ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
145 150 155 160
ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
165 170 175
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
180 185 190
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
195 200 205

tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
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 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr
245 250 255

Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser
260 265 270

Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly
275 280 285

Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg
290 295 300

Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly
305 310 315 320

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly
325 330 335
Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys
340 345 350
Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu
355 360 365
Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
370 375 380
Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
385 390 395 400
Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
405 410 415
Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
420 425 430
Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
435 440 445
Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
450 455 460
Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
465 470 475 480
Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu
485 490 495
Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly
500 505 510
Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp
515 520 525
Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val

530 535 540
Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Arg Pro Tyr
545 550 555 560
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
565 570 575
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
580 585 590
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
595 600 605
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
610 615 620
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
625 630 635 640
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
645 650 655
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
660 665 670
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
675 680 685
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
690 695 700
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
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<211> 2241

<212> DNA

<213> *Montipora. sp*

<400> 50

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15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

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25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35

40

45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

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55

60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

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70

75

80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

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90

95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

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105

110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc 720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240
gga ctc aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc 768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr
245 250 255
gcg ggc ccg ctg tac gac gaa gtc gat aag gat ccg atg gcc tcc tcc 816

Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser
260 265 270
gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc 864
Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly
275 280 285
tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc 912
Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg
290 295 300
ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc 960
Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly
305 310 315 320
ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc 1008
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly
325 330 335
tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag 1056
Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys
340 345 350
ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag 1104
Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu
355 360 365
gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc 1152
Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
370 375 380
gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac 1200
Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
385 390 395 400
ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag 1248

Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
 405 410 415
 cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg 1296
 Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
 420 425 430
 ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc 1344
 Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
 435 440 445
 tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac 1392
 Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
 450 455 460
 atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa 1440
 Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
 465 470 475 480
 cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc tcc gga ctc 1488
 Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu
 485 490 495
 aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc gcg ggc 1536
 Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly
 500 505 510
 ccg ctg tac gac gaa gtc ggt aag gat ccg atg gcc tcc tcc gag gac 1584
 Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp
 515 520 525
 gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc tcc gtg 1632
 Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val
 530 535 540
 aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac 1680

Asn Gly His Glu Phe Glu Glu Ile Glu Gly Glu Gly Arg Pro Tyr
 545 550 555 560
 gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg 1728
 Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
 565 570 575
 ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag 1776
 Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
 580 585 590
 gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc 1824
 Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
 595 600 605
 ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc 1872
 Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
 610 615 620
 ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc 1920
 Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
 625 630 635 640
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 Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
 645 650 655
 gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg 2016
 Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
 660 665 670
 tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag 2064
 Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
 675 680 685
 ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg 2112

Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
690 695 700
gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag 2160
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
705 710 715 720
ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac 2208
Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
725 730 735
gag cgc gcc gag ggc cgc cac tcc acc ggc gcc 2241
Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
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<211> 507
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp
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Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
35 40 45
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
50 55 60
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
65 70 75 80
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

	85	90	95
Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
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Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
	115	120	125
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
	130	135	140
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
	145	150	155
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
	165	170	175
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
	180	185	190
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
	195	200	205
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
	210	215	220
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
	225	230	235
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
	245	250	255
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	260	265	270
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser			
	275	280	285
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val			
	290	295	300

Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr
305 310 315 320
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu
325 330 335
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile
340 345 350
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser
355 360 365
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly
370 375 380
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe
385 390 395 400
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro
405 410 415
Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu
420 425 430
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys
435 440 445
Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys
450 455 460
Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys
465 470 475 480
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Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
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<212> DNA

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10

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp

20

25

30

ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144

Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile

35

40

45

ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc 192

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser

50

55

60

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

65

70

75

80

atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

85

90

95

acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336

Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met

100

105

110

aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln

115 120 125
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
130 135 140
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
145 150 155 160
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
165 170 175
tac aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
180 185 190
aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc 624
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
195 200 205
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
210 215 220
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 720
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
225 230 235 240
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
245 250 255
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 816
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

260 265 270
tcc tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agt 864
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser
275 280 285
gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc acg gtc 912
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val
290 295 300
aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct tac 960
Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr
305 310 315 320
gag gga gag cag aca gta aag ctc act gtc acc aag ggt gga cct ctg 1008
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu
325 330 335
cca ttt gct tgg gat att tta tca cca ctg ttt cag tac gga agc ata 1056
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile
340 345 350
cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag cag tca 1104
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser
355 360 365
ttc cct gag gga tat aca tgg gag agg acc atg aac ttt gaa gat ggt 1152
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly
370 375 380
gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt ttc 1200
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe
385 390 395 400
atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc aat gga cct 1248
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro

405	410	415
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Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu		
420	425	430
ttt gca cga gat gga atg ctg ata gga aac gat tat atg gct ctg aag 1344		
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys		
435	440	445
ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct act tac aag 1392		
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450	455	460
gca aag aag cct gtg agg atg cca ggg tat cac tat att gac cgc aaa 1440		
Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys		
465	470	475
ctg gat gta acc agt cac aac agg gat tac aca tct gtt gag cag tgt 1488		
Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys		
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35 40 45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
50 55 60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
65 70 75 80

Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
85 90 95

Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
100 105 110

Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
115 120 125

Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
130 135 140

Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro
145 150 155 160

Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
165 170 175

Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
180 185 190

Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
195 200 205

Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr
210 215 220

Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
225 230 235 240

Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser
245 250 255
Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys
260 265 270
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
275 280 285
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
290 295 300
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
305 310 315 320
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly
325 330 335
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
340 345 350
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
355 360 365
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
370 375 380
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
385 390 395 400
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
405 410 415
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
420 425 430
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
435 440 445
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu

450 455 460
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp
20 25 30
ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
35 40 45
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
50 55 60
gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
65 70 75 80

ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag 288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
85 90 95
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
100 105 110
gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac 384
Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
115 120 125
ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
130 135 140
ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct 480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro
145 150 155 160
ccc aat gga cct gtt atg cag aag aca cag ggc tgg gaa ccc agc 528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
165 170 175
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
180 185 190
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
195 200 205
tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat 672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr
210 215 220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
225 230 235 240
gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tcc 768
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser
245 250 255
tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agc aag 816
Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys
260 265 270
ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac 864
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
275 280 285
ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc 912
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
290 295 300
gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc 960
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
305 310 315 320
aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc 1008
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly
325 330 335
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Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
340 345 350
ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc 1104
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
355 360 365

ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag 1152
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
370 375 380
ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 1200
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
385 390 395 400
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 1248
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
405 410 415
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 1296
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
420 425 430
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1344
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435 440 445
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1392
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
450 455 460
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1440
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
465 470 475 480
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1488
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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<212> PRT

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35

40

45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser

50

55

60

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

65

70

75

80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

85

90

95

Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met

100

105

110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln

115

120

125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala

130

135

140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys

145

150

155

160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu

165

170

175

Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
180 185 190
Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly
195 200 205
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
210 215 220
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
225 230 235 240
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
245 250 255
Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile
260 265 270
Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
275 280 285
Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln
290 295 300
Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
305 310 315 320
Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala
325 330 335
Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe
340 345 350
Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu
355 360 365
Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
370 375 380
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp			
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ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144			
Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile			
35	40	45	
ctg gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc 192			
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser			
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ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240			
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe			
65	70	75	80
atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288			
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr			
85	90	95	
acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336			

Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
100 105 110
aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
115 120 125
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
130 135 140
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
145 150 155 160
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
165 170 175
tac aac tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
180 185 190
aac ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc 624
Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly
195 200 205
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
210 215 220
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Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
225 230 235 240
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
245 250 255

tgc gtc acc gcc gcc cgc atg cat gac caa ctg aca gaa gag cag att 816
Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile
260 265 270

gca gag ttc aaa gaa gcc ttc tca tta ttc gac aag gat ggg gac ggc 864
Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
275 280 285

acc atc acc aca aag gaa ctt ggc acc gtt atg agg tcg ctt gga caa 912
Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln
290 295 300

aac cca acg gaa gca gaa ttg cag gat atg atc aat gaa gtc gat gct 960
Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
305 310 315 320

gat ggc aat gga acg att tac ttt cct gaa ttt ctt act atg atg gct 1008
Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala
325 330 335

aga aaa atg aag gac aca gac agc gaa gag gaa atc cga gaa gca ttc 1056
Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe
340 345 350

cgt gtt ttt gac aag gat ggg aac ggc tac atc agc gct gct gaa tta 1104
Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu
355 360 365

cgt cac gtc atg aca aac ctc ggg gag aag tta aca gat gaa gaa gtt 1152
Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
370 375 380

gat gaa atg ata agg gaa gca gat atc gat ggt gat ggc caa gta aac 1200

Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn
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 Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp
 20 25 30
 Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn
 35 40 45
 Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Ser
 50 55 60
 Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr
 65 70 75 80
 Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly
 85 90 95
 Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr
 100 105 110
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe
 115 120 125
 Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp

130 135 140
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met
145 150 155 160
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile
165 170 175
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe
180 185 190
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro
195 200 205
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp
210 215 220
Tyr Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe
225 230 235 240
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His
245 250 255
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr
260 265 270
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
275 280 285
<210> 58
<211> 864
<212> DNA
<213> *Montipora. sp*
<400> 58
atg cgg ggt tct cat cat cat cat cat ggt atg gct agc atg act 48
Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20 25 30

ccc aag agg cgc tgg aag aaa aac ttc att gcc gtc agc gct gcc aac 144
Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn

35 40 45

cgg ttc aag aag atc tcc agc tcc ggg gca ctg gga ggt gga ggt agt 192
Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Ser

50 55 60

gag ctc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat 240
Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr

65 70 75 80

atg tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga 288
Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly

85 90 95

aaa gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc 336
Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr

100 105 110

aag ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt 384
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe

115 120 125

cag tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat 432
Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp

130 135 140

tat gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg 480
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met

145 150 155 160

aac ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc 528
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile
165 170 175
caa ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt 576
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe
180 185 190
cct ccc aat gga cct gtt atg cag aag aac aca cag ggc tgg gaa ccc 624
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro
195 200 205
agc act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat 672
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp
210 215 220
tat atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt 720
Tyr Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe
225 230 235 240
aaa tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac 768
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His
245 250 255
tat att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca 816
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr
260 265 270
tct gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 864
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
275 280 285
<210> 59
<211> 33
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 59

ccagagatga agatgaggta ctacatggac ggc 33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 60

catgagttca caattgaagg tgaaggc 27

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 61

gaaggcacag gcagaccta cgaggga 27

<210> 62

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 62
ccaatgcctt tcgcgtttga ctttagtg 27
<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 63
ttagtgtcac acgtgttctg ttacggc 27
<210> 64
<211> 27
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 64
gaaaggtcgt tggagttcga agatgg 27
<210> 65
<211> 30
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 65
gaagatggtg ggtccgcttc agtcagtgcg 30
<210> 66

<211> 34
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 66
agccttagag gaaacacctt ctaccacaaa tcca 34
<210> 67
<211> 32
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 67
caaatccaaa ttactgggg ttaactttcc tg 32
<210> 68
<211> 30
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 68
gccgatggtc ctatcatgca aaacccaaagt 30
<210> 69
<211> 45
<212> DNA
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<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 69

gccgatggtc ctatcatgca aaaccaaagt gttgattggg agcca 45

<210> 70

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 70

gagaaaatta ctgccagcga cggagttctg aag 33

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 71

gatgttacga tgtacctaaa acttgaagga ggccggcaatc ac 42

<210> 72

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 72

cttaaaatgc caggaagcca ttacatcagc catgcctcg tcagg 45
<210> 73
<211> 34
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 73

gatgcagtag ctcattccct cgagcaccac cacc 34
<210> 74
<211> 21
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 74

gaaggrtgyg tcaayggrrca y 21
<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 75

acvggdccat ydgvaagaaa rtt 23
<210> 76
<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 76

ggccacgcgt cgactagtagtac gggiiiggii gggiig 36

<210> 77

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 77

ctcaggaaat gactgcttta cat 23

<210> 78

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 78

ggccacgcgt cgactagtagtac 20

<210> 79

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA
<400> 79

gtcttcaggg tacttggtga 20

<210> 80

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
<400> 80

atgtaaagca gtcattccct gag 23

<210> 81

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
<400> 81

cccgatccg accatggcta cttggtaa aga 33